TRANSFAC® Matrix Report Overview

BIOBASE
BIOLOGICAL DATABASES

| M02006 | Matrix: V$GATA5_Q4 - GATA-5 |
| | Type: factor-specific matrix |

Positional Weight Matrix

Matrix overview

Sequence logo :

| Nucleotide position frequency | | | | | | Nucleotide position frequency | | | | |
A	C	G	T	Consensus		A	C	G	T	Consensus
4	0	0	13	T		4	5	4	4	N
17	0	0	0	A		11	0	2	4	A
0	0	0	17	T		1	0	16	0	G
0	16	0	1	C		17	0	0	0	A
4	2	0	11	T		0	0	0	17	T
4	4	5	4	N		13	0	0	4	A

Experimental basis for positional weight matrix construction

Transcription factors :

Human GATA-5
Mouse GATA-5
Rat GATA-5
Mammalia GATA-5
Gallus gallus GATA-5
Xenopus laevis GATA-5A
Xenopus laevis GATA-5B

Number of sites represented in matrix:
- Human GATA-5: 1
- Xenopus laevis GATA-5A: 1
- Mouse GATA-5: 5
- Rat GATA-5: 4
- Xenopus laevis GATA-5B: 1
- Mammalia GATA-5: 7
- Gallus gallus GATA-5: 1

Site alignment :

Sequence	Transcription factors	Bound Gene	Experimental evidence	Experimental source	References
TATCTg	● GATA-5A(x) ○ GATA-5B(x)	FABPI(x)	CI DM FA FO GS SS P BE OT	rec(m.s.-Caco -2) [more…]	[5] [14]
AATCTC	◐ GATA-5(m) ○ GATA-5(r)	Tnnc1(m)	CI DM FA FO GS SS P BE OT	rec(mouse-NIH3T3) [more…]	[11] [13] [18] [19] [20]
TATCAa	◐ GATA-5(m)	Nppa(r)	CI DM FA FO GS SS P BE OT	heart, neonatal + ET-1 [more…]	[4] [8] [9] [11] [12]
TATCTA	○ GATA-5(h)	Lct(r)	CI DM FA FO GS SS P BE OT	rec(rat-QT6) [more…]	[10]
AATCTt	○ GATA-5(m.s.)	NOX1(h)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[3]
AATCTT	○ GATA-5(m.s.)	NOX1(h)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[3]
TATCTA	○ GATA-5(m.s.)	NOX1(h)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[3]
TATCAA	○ GATA-5(m.s.)	NOX1(h)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[3]
TATCTa	○ GATA-5(m.s.)	LCT(h)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[5] [16]
TATCAc	○ GATA-5(m.s.)	LCT(h)	CI DM FA FO GS SS P BE OT	rec(mammalian-in vitro)	[5]
TATCCC	◐ GATA-5(m)	Slc9a3(r)	CI DM FA FO GS SS P BE OT	Caco-2 [more…]	[7]
TATCCC	◐ GATA-5(m) ◐ GATA-5(r)	Bmyo(r)	CI DM FA FO GS SS P BE OT	neonatal cardiac myocytes [more…]	[13] [17]
TATCTT	○ GATA-5(c)	Chrm2(m)	CI DM FA FO GS SS P BE OT	heart, chick [more…]	[15]
TATCAT	◐ GATA-5(m)	Gnrh1(r)	CI DM FA FO GS SS P BE OT	GT1-7	[1]
AATCTg	◐ GATA-5(r)	Smarca2(m)	CI DM FA FO GS SS P BE OT	P-19 [more…]	[2]
TATTTT	◐ GATA-5(r)	Smarca2(m)	CI DM FA FO GS SS P BE OT	P-19 [more…]	[2]
TATCTt	○ GATA-5(m.s.)	Smad7(m)	CI DM FA FO GS SS P BE OT	HepG2 [more…]	[6]

Matrix Category : matrix compiled from individual genomic sites

Application details : compiled and aligned by BIOBASE; sites quality 4 or better

Number of sequences used : 17

Related matrices

Related family matrices	Consensus binding sequence derived from Positional Weight Matrix	Category method
GATA	V$GATA_Q6	matrix compiled from individual genomic sites

Identifiers

BIOBASE accession : M02006

References (22 entries)

[1] PMID 18259093. Leclerc, G. M., Bose, S. K., Boockfor, F. R., Specific GATA-binding elements in the GnRH promoter are required for gene expression pulse activity: role of GATA-4 and GATA-5 in this intermittent process. Neuroendocrinology 88 (1) 1-16 (2008).

[2] PMID 18082132. Differentiation-specific expression of chromatin remodeling factor BRM. Book 366 827-833 (2008).

[3] PMID 18005670. Valente, A. J., Zhou, Q., Lu, Z., He, W., Qiang, M., Ma, W., Li, G., Wang, L., Banfi, B., Steger, K., Krause, K. H., Clark, R. A., Li, S., Regulation of NOX1 expression by GATA, HNF-1alpha, and Cdx transcription factors. Free Radic Biol Med 44 (3) 430-43 (2008).

[4] PMID 15574430. Interleukin-18 is a pro-hypertrophic cytokine that acts through a phosphatidylinositol 3-kinase-phosphoinositide-dependent kinase-1-Akt-GATA4 signaling pathway in cardiomyocytes. Book 280 4553-4567 (2005).

[5] PMID 15178553. van Wering, H. M., Bosse, T., Musters, A., de Jong, E., de Jong, N., Hogen Esch, C. E., Boudreau, F., Swain, G. P., Dowling, L. N., Montgomery, R. K., Grand, R. J., Krasinski, S. D., Complex regulation of the lactase-phlorizin hydrolase promoter by GATA-4. Am J Physiol Gastrointest Liver Physiol 287 (4) G899-909 (2004).

[more . . .]

M02006: V$GATA5_Q4

1   The original and reverse complement nucleotide position frequency and sequence logo are both presented, making it easy to compare binding sites regardless of strand orientation.

2   The new bar graph makes it easy to see at-a-glance how many binding sites each transcription factor contributed to the compiled matrix.

3   The updated site alignment table provides (when applicable) detailed information for each of the binding sites used to compile the matrix including the binding factor, the bound gene, the experimental method and system used to determine binding, plus links to the reference(s) from which the site was taken.

4 **5**   The new matrix category classification system (4) and related factor-specific and family matrices (5) allows you to easily identify how a matrix was constructed and to compare it to other matrices within TRANSFAC and public domain offerings.

6   The reference section lists the complete set of supporting references.

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